

Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu  
180 185 190

Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln  
195 200 205

Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val  
210 215 220

Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His  
225 230 235

<210> 1  
<211> 988  
<212> DNA  
<213> Homo sapiens

<220>  
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1 5

agc cca aca acc tat ctc ctc ctg ctg ctg ctg ctg agc tcg gga ctc 101  
Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Ser Ser Gly Leu  
10 15 20

agt ggg acc cag gac tgc tcc ttc caa cac agc ccc atc tcc tcc gac 149  
Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp  
25 30 35 40

ttc gct gtc aaa atc cgt gag ctg tct gac tac ctg ctt caa gat tac 197  
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
45 50 55

cca gtc acc gtg gcc tcc aac ctg cag gac gag gag ctc tgc ggg ggc 245  
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly  
60 65 70

ctc tgg cgg ctg gtc ctg gca cag cgc tgg atg gag cgg ctc aag act 293  
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr  
75 80 85

gtc gct ggg tcc aag atg caa ggc ttg ctg gag cgc gtg aac acg gag 341  
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu  
90 95 100

ata cac ttt gtc acc aaa tgt gcc ttt cag ccc ccc ccc agc tgt ctt 389  
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu  
105 110 115 120

cgc ttc gtc cag acc aac atc tcc cgc ctc ctg cag gag acc tcc gag 437  
Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu  
125 130 135

ggccccattt acccaactct gaacaaagcc cccg 988

<400> 4

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37

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 <211> 77  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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 cttcgcccg tgcttg 77

<210> 6  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: constructed  
 oligonucleotide

<400> 6  
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 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: constructed  
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<400> 7  
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<210> 8  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
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Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
 35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

<210> 9

<211> 209

<212> PRT

<213> Homo sapiens

<400> 9

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Thr  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

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<211> 212  
<212> PRT  
<213> Homo sapiens

<400> 10  
His Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser  
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Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp  
20 25 30

Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly  
35 40 45

Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys  
50 55 60

Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr  
65 70 75 80

Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys  
85 90 95

Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser  
100 105 110

Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser  
115 120 125

Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro  
130 135 140

Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln  
145 150 155 160

Pro Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu  
165 170 175

Ala Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro  
180 185 190

Arg Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu  
195 200 205

Leu Val Glu His  
210

<210> 11

<211> 209

<212> PRT

<213> Homo sapiens

<400> 11

Thr Gln Asp Cys Ser Phe Gln Tyr Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
 195 200 205

His

<210> 12  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
 1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Phe Leu Gln Asp Tyr Pro Val  
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
 35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
 50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
 65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
 85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
 100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
 115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
 130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
 145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
 165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
 180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
 195 200 205

His

<210> 13  
 <211> 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
 1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Pro Gln Asp Tyr Pro Val  
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
 35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
 50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
 65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
 85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
 100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
 115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
 130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
 145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Ala Ala Ala  
 165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
 180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
 195 200 205

His

&lt;210&gt; 14

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
 1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
 20 25 30

His

<400> 15

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Thr Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

<210> 16

<211> 209

<212> PRT

<213> Homo sapiens

<400> 16

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Arg Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
 130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
 145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
 165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
 180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
 195 200 205

His

<210> 17

<211> 209

<212> PRT

<213> Homo sapiens

<400> 17

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
 1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
 35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
 50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
 65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
 85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
 100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Arg Cys Leu  
 115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
 130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
 145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
 165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
 180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
 195 200 205

His

<210> 18

<211> 209

<212> PRT

<213> Homo sapiens

<400> 18

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
 1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
 35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
 50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
 65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
 85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
 100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
 115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
 130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
 145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
 165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
 180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
 195 200 205

His

<210> 19  
 <211> 137  
 <212> PRT  
 <213> Murine

<400> 19  
 Thr Pro Asp Cys Tyr Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys  
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Val Lys Phe Arg Glu Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val  
 20 25 30

Thr Val Ala Val Asn Leu Gln Asp Glu Glu Lys His Cys Lys Ala Leu  
 35 40 45

Trp Ser Leu Phe Leu Ala Gln Arg Trp Ile Glu Gln Leu Lys Thr Val  
 50 55 60

Ala Gly Ser Lys Met Gln Thr Leu Leu Glu Asp Val Asn Thr Glu Ile  
 65 70 75 80

His Phe Val Thr Ser Cys Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg  
 85 90 95

Phe Val Gln Thr Asn Ile Ser His Leu Leu Lys Asp Thr Cys Thr Gln  
 100 105 110

Leu Leu Ala Leu Lys Pro Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser  
 115 120 125

Arg Cys Leu Glu Val Gln Cys Gln Pro  
 130 135

<210> 20  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu  
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Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln  
 20 25 30

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys  
 35 40 45

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr  
 50 55 60

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu  
 65 70 75 80

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu  
85 90 95

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln  
100 105 110

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu  
115 120 125

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala  
130 135 140

Glu Cys Ser Ser Gln  
145

145  
140  
135  
130  
125  
120  
115  
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: GRADDIS, Thomas J.  
MCGREW, Jeffrey T.

(ii) TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner, L.L.P.

(B) STREET: 1300 I Street, N.W.

(C) CITY: Washington

(D) STATE: D.C.

(E) COUNTRY: USA

(F) ZIP: 20005-3315

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Fordis, Jean B.

(B) REGISTRATION NUMBER: 32,984

(C) REFERENCE/DOCKET NUMBER: 03260.0028-00000

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-408-4000

(B) TELEFAX: 202-408-4400

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu  
1 5 10 15

Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe  
20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
50 55 60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
65 70 75 80

Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
85 90 95

Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
100 105 110

Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
115 120 125

Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
130 135 140

Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
145 150 155 160

Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala  
165 170 175

Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu  
180 185 190

Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln  
195 200 205

Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val  
210 215 220

Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA GCC  
TGG 53

Met Thr Val Leu Ala Pro Ala Trp  
1 5

AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG AGC TCG GGA CTC  
101

Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu  
10 15 20

AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC GAC  
149

Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp  
25 30 35 40

TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT TAC  
197

Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr

45

50

55

CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG GGC

245

Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly

60

65

70

CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG ACT

293

Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr

75

80

85

GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG GAG

341

Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu

90

95

100

ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT CTT

389

Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu

105

110

115

120

CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG

437

Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu

125

130

135

CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG

485

Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg

140

145

150

TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA

533

Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro

155

160

165

TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC

581

Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro

170

175

180

CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC

629

Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala  
185 190 195 200

GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC  
CGC

677

Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg  
205 210 215

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT  
725

Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu  
220 225 230

GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTAAACAAC  
774

Val Glu His  
235

GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG  
CACACAGAGG 834

GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA  
GAGGCCGGTC 894

CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA  
ATCCAGCACC 954

GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG

988

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTAGGTACC TTTGGATAAA AGACTCAGTG GGACCAGGAC

40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATATGGATCC CTACGGGGCT GTGGCCTCCA GGGGCCG

37

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCTCCTGCAG GAGACCTCCG AGCAGCTGGT GGCGCTGAAG CCCTGGATCA

CTCGCCAGAA 60

CTTCGCCCCGG TGCCTGG

77

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGGATAAAAG ACACAGTGGG ACCCAGGACT GCTCCTTCCA ATACAG  
46

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGGATAAAAG ACACAGTGGG ACCCAGGACT GCTCCTTCCA ATACAG  
46

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Gln Asp Cys Ser Phe Gln Arg Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Thr  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu

115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

His Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser  
1 5 10 15

Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp  
20 25 30

Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly  
35 40 45

Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys  
50 55 60

Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr

65                      70                      75                      80

Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys  
                    85                      90                      95

Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser  
                    100                      105                      110

Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser  
                    115                      120                      125

Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro  
                    130                      135                      140

Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln  
145                      150                      155                      160

Pro Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu  
                    165                      170                      175

Ala Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro  
                    180                      185                      190

Arg Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu  
                    195                      200                      205

Leu Val Glu His  
                    210

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Gln Asp Cys Ser Phe Gln Tyr Ser Pro Ile Ser Ser Asp Phe Ala  
1                      5                      10                      15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Phe Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Pro Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala

165

170

175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Thr Pro Arg Pro Gly  
 180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
 195 200 205

His

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
 1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
 35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
 50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
 65 70 75 80

Phe Val Thr Glu Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
 85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
 100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Thr Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Arg Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

## (2) INFORMATION FOR SEQ ID NO:17:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Glu Leu Cys Gly Gly Leu Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala Ala Ala  
165 170 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205

His

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190  
Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205  
His